

BLAST

Basic Local Alignment Search Tool

- Your search parameters were adjusted to search for a short input sequence.

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Protein Sequence (8 letters)

residues 73-80 of SEQ ID NO: 12

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

|cl|27776

|cl|27776

Description

None

Molecule type

amino acid

Query Length

8

Database Name

nr

Description

All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

Program

BLASTP 2.2.22+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Other reports: [Search Summary](#) [Taxonomy reports](#) [Multiple alignment](#) **NEW**

Search Parameters

Program	blastp
Word size	2
Expect value	200000
Hitlist size	100
Gapcosts	9,1
Matrix	PAM30
Threshold	11
Filter string	F
Genetic Code	1
Window Size	40

Database

Posted date	Jan 3, 2010 5:44 PM
Number of letters	3,505,793,397
Number of sequences	10,274,250
Entrez query	none

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.368907	0.294
K	0.286243	0.11
H	1.92795	0.61

Results Statistics

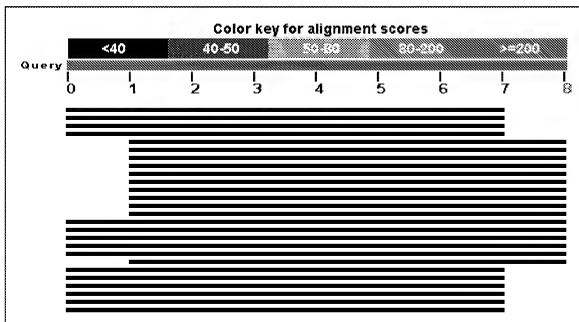
Length adjustment	0
Effective length of query	8
Effective length of database	3505793397
Effective search space	28046347176
Effective search space used	28046347176

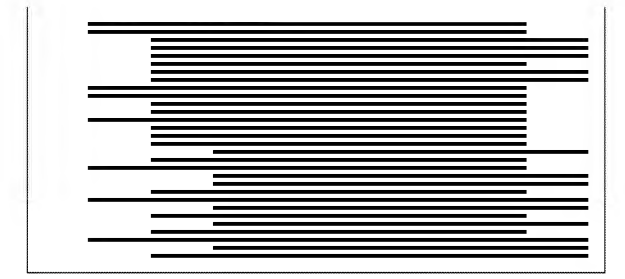
[Graphic Summary](#)[Show Conserved Domains](#)

No putative conserved domains have been detected

**Distribution of 101 Blast Hits on the Query Sequence**

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.





Descriptions

E	Sequences producing significant alignments:	Score	
		(Bits)	Value
emb CAA46601.1	urinary plasminogen activator [Rattus norvegi...	25.2	708
ref NP_047171.3	plasminogen activator, urokinase [Rattus nor...	25.2	708
ep P29596.1 OPQN_RAT	RecName: Full=Urokinase-type plasminogen...	25.2	708
ref NP_032999.1	plasminogen activator, urokinase [Mus muscul...	25.2	708
gb ACX36365.1	middle S protein [Hepatitis B virus] >gb ACX36...	24.8	949
gb ACX36357.1	middle S protein [Hepatitis B virus]	24.8	949
gb AEU97123.1	S protein [Hepatitis B virus]	24.8	949
gb AEU17003.1	surface antigen [Hepatitis B virus]	24.8	949
gb EAG12008.1	S protein [Hepatitis B virus]	24.8	949
ref XP_001459163.1	hypothetical protein [Paramecium tetraure...	24.8	949
gb AAK59309.1	HBsAg [Hepatitis B virus]	24.8	949
gb AAK59315.1	HBsAg [Hepatitis B virus]	24.8	949
gb AAK61740.1	51C surface protein [Paramecium tetraurelia]	24.8	949
gb AAK65562.1	HBsAg [Hepatitis B virus]	24.8	949
gb AAU13661.1	surface antigen [Hepatitis B virus]	23.5	2294
gb ACE45647.1	truncated S protein [Hepatitis B virus]	23.1	3077
gb ACE45646.1	truncated large S protein [Hepatitis B virus]	23.1	3077
ref XP_001759707.1	hypothetical protein [Monosiga brevicolli...	23.1	3077
ref NP_002032075.1	GE11868 [Drosophila yakuba] >gb EDW91787...	22.7	4129
gb EFA75884.1	hypothetical protein PPL10456 [Polysphondyliu...	22.3	5541
ref XP_003006388.1	Cof-like hydrolase [Dickeya zeae Ech1591]...	22.3	5541
gb EER2595.1	BNR/Asp-box repeat domain-containing protein, ...	22.3	5541
ref XP_002368431.1	sortilin, putative [Toxoplasma gondii] ME4...	22.3	5541
ref NP_00144615.1	hypothetical protein LOC100277631 [Zea ma...	22.3	5541
ref XP_001742225.1	hypothetical protein [Monosiga brevicolli...	22.3	5541
ref XP_001764053.1	predicted protein [Physcomitrella patens ...	22.3	5541
ref XP_001669438.1	FAD dependent oxidoreductase [Pseudomonas...	22.3	5541
ref XP_001756901.1	predicted protein [Physcomitrella patens ...	22.3	5541
ref NP_638662.1	hypothetical protein DDB_G0283853 [Dictyoste...	22.3	5541
ref XP_638662.1	hypothetical protein DDB_G0283869 [Dictyoste...	22.3	5541
ref XP_638663.1	hypothetical protein DDB_G0283787 [Dictyoste...	22.3	5541
gb EER62515.1	hypothetical protein PANDA_005925 [Ailuropoda ...	21.8	7434
gb EER62092.1	hypothetical protein PPL_05237 [Polysphondyliu...	21.8	7434
gb EER62091.1	carbohydrate-binding domain-containing protein...	21.8	7434
ref XP_00141614.1	pectinesterase [Ruminococcus flavefaciens ...	21.8	7434
emb CER16504.1	peridic tryptophan protein 2, putative; pred...	21.8	7434
ref NP_002444714.1	hypothetical protein SORBIDRAFT_07g026515...	21.8	7434
ref XP_002578344.1	transcription initiation factor brfl [Sch...	21.8	7434
ref YP_002756665.1	lipoprotein [Escherichia coli] >gb ACL520...	21.8	7434
ref XP_002731228.1	cytochrome C family protein [Persephonella...	21.8	7434
ref XP_001013897.2	hypothetical protein THERM_01486710 [Tet...	21.8	7434
ref XP_002746320.1	DNA topoisomerase (ATP-hydrolyzing) [Opitu...	21.8	7434
gb EER55730.1	hypothetical protein OsJ_04192 [Oryza sativa J...	21.8	7434
ref XP_002590185.1	predicted protein [Thalassiosira pseudona...	21.8	7434
ref YP_002418785.1	putative lipoprotein [Escherichia coli] >...	21.8	7434
ref XP_002430137.1	hypothetical protein IscW_ISCW011495 [Ixo...	21.8	7434
ref XP_002596165.1	hypothetical protein BRAFLDRAFT_123314 [B...	21.8	7434
ref XP_002612022.1	hypothetical protein BRAFLDRAFT_86993 [Br...	21.8	7434

ref XP_003613102.1	hypothetical protein BRAFLDRAFT_89993 [Br...	21.8	7434
ref XP_003124394.1	PREDICTED: similar to integrin beta Hrl [...	21.8	7434
dbj BA665492.1	unnamed protein product [Homo sapiens]	21.8	7434
gb AA166315.1	LOC100158602 protein [Xenopus (Silurana) tropi...	21.8	7434
ref XP_001912476.1	unnamed protein product [Podospora anseri...	21.8	7434
ref XP_001907985.1	unnamed protein product [Podospora anseri...	21.8	7434
ref XP_001770309.1	predicted protein [Physcomitrella patens ...	21.8	7434
ref XP_001775575.1	p300/CBP acetyltransferase-related protei...	21.8	7434
ref XP_001785357.1	p300/CBP acetyltransferase-related protei...	21.8	7434
ref XP_001994459.1	hypothetical protein PEPMIC_01220 [Parvimo...	21.8	7434
ref XP_003736.2	hypothetical protein NCU03244 [Neurospora cr...	21.8	7434
ref XP_001502309.1	PREDICTED: fibrillin 1 [Equus caballus]	21.8	7434
ref XP_001894392.1	hypothetical protein MDG893_13589 [Marinob...	21.8	7434
gb EDL00069.1	fibrillin 1, isoform CRA_a [Rattus norvegicus]...	21.8	7434
gb EDL00071.1	fibrillin 1, isoform CRA_b [Rattus norvegicus]	21.8	7434
gb EDL00139.1	fibrillin 1, isoform CRA_a [Mus musculus] >gb ...	21.8	7434
ref XP_001393188.1	hypothetical protein An08g10840 [Aspergil...	21.8	7434
ref XP_001369848.1	PREDICTED: hypothetical protein [Monodelp...	21.8	7434
ref XP_001369848.1	hypothetical protein OsI_04550 [Oryza sativa I...	21.8	7434
ref XP_001442593.1	hypothetical protein [Paramecium tetraure...	21.8	7434
ref XP_001453530.1	conserved protein [Microscilla marina ATCC...	21.8	7434
gb EAW77353.1	fibrillin 1 (Marfan syndrome), isoform CRA_a [...	21.8	7434
ref NP_000129.3	fibrillin 1 precursor [Homo sapiens] >sp P35...	21.8	7434
ref NP_022019.2	fibrillin 1 [Mus musculus] >emb CAM22806.1 ...	21.8	7434
ref XP_0060476.1	drug/metabolite exporter family transporter ...	21.8	7434
ref XP_001192266.1	PREDICTED: fibrillin 1 [Pan troglodytes]	21.8	7434
ref NP_001044999.1	Os0lg0865600 [Oryza sativa (japonica cult...	21.8	7434
ref XP_0074600.3	PREDICTED: similar to family with sequence s...	21.8	7434
ref XP_002100.3	PREDICTED: similar to CG16791-PA [Apis melli...	21.8	7434
ref XP_001106609.1	PREDICTED: estrogen-related receptor beta...	21.8	7434
ref NP_001113107.1	PREDICTED: similar to fibrillin 1 precurs...	21.8	7434
ref XP_001306357.1	hypothetical protein RED65_16411 [Oceanoba...	21.8	7434
ref XP_0011706.1	PREDICTED: similar to Fibrillin-1 precursor ...	21.8	7434
ref XP_0035468.2	PREDICTED: similar to Fibrillin-1 precursor ...	21.8	7434
dbj EAD92077.1	fibrillin 1 variant [Homo sapiens]	21.8	7434
dbj EAD91907.1	bHLH transcription factor-like protein [Oryza...	21.8	7434
ref AA194187.1	PilL [Escherichia coli]	21.8	7434
ref YP_006679.1	lipoprotein [Escherichia coli] >gb AAL18827....	21.8	7434
gb AAL05516.1	PilL [Escherichia coli]	21.8	7434
emb CAD19195.1	novel protein similar to MHC class II beta ch...	21.8	7434
ref XP_001030643.1	hypothetical protein THERM_01006510 [Tet...	21.8	7434
gb AAC62317.1	mutant fibrillin-1 [Mus musculus]	21.8	7434
gb AAA64217.1	fibrillin-1 [Mus musculus]	21.8	7434
ref XP_001733.1	PREDICTED: similar to Fibrillin-1 precursor ...	21.8	7434
ref XP_001745.1	PREDICTED: similar to Fibrillin-1 precursor ...	21.8	7434
ref XP_001745.1	PREDICTED: similar to Fibrillin-1 precursor ...	21.8	7434
ref NP_114013.1	fibrillin 1 [Rattus norvegicus] >gb AAD34438...	21.8	7434
dbj EAD16739.1	fibrillin 1 [Homo sapiens]	21.8	7434
ref XP_003613102.1	C. briggsae CBR-LAM-1 protein [Caenorhabd...	21.8	7434

```

>ref|NP_001001771.1| fibrillin 1 precursor [Sus scrofa] >sp|Q9... 21.8 7434
>prf|11713408A| fibrillin 21.8 7434
>sp|Q41554.1|FBN1_MOUSE RecName: Full=Fibrillin-1; Flags: Prec... 21.8 7434

```

Alignments [Select All](#) [Get selected sequences](#) [Distance tree of results](#) [Multiple alignment](#) [NEW](#)

```

>emb|CAA46601.1| G urinary plasminogen activator [Rattus norvegicus]
Length=432

GENE ID: 25619 Plau | plasminogen activator, urokinase [Rattus norvegicus]
(Over 10 PubMed links)

```

Score = 25.2 bits (52), Expect = 708
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

```

Query 1 RISTGQC 7
      RISTGQC
Sbjct 283 RISTGQC 289

```

```

>ref|NP_037217.3| UG plasminogen activator, urokinase [Rattus norvegicus]
gb|AAI05860.1| G Plasminogen activator, urokinase [Rattus norvegicus]
gb|EDL86256.1| G rCG41849 [Rattus norvegicus]
Length=432

```

GENE ID: 25619 Plau | plasminogen activator, urokinase [Rattus norvegicus]
(Over 10 PubMed links)

Score = 25.2 bits (52), Expect = 708
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

```

Query 1 RISTGQC 7
      RISTGQC
Sbjct 283 RISTGQC 289

```

```

>sp|P29598.1|UROK_RAT G RecName: Full=Urokinase-type plasminogen activator; Shor
Short=U-plasminogen activator; Contains: RecName: Full=Urokinase-type
plasminogen activator long chain A; Contains: RecName:
Full=Urokinase-type plasminogen activator short chain
A; Contains: RecName: Full=Urokinase-type plasminogen activator
chain B; Flags: Precursor
emb|CAA45028.1| G urikinasе-type plasminogen activator [Rattus norvegicus]
Length=432

```

GENE ID: 25619 Plau | plasminogen activator, urokinase [Rattus norvegicus]
(Over 10 PubMed links)

Score = 25.2 bits (52), Expect = 708
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

```

Query 1 RISTGQC 7
      RISTGQC
Sbjct 283 RISTGQC 289

```

```

>ref|NP_032899.1| UG plasminogen activator, urokinase [Mus musculus]
sp|P06869.1|UROK_MOUSE G RecName: Full=Urokinase-type plasminogen activator; Sh
activator; Short=uPA; Contains: RecName: Full=Urokinase-type
plasminogen activator long chain A; Contains: RecName:
Full=Urokinase-type plasminogen activator short chain
A; Contains: RecName: Full=Urokinase-type plasminogen activator
chain B; Flags: Precursor
emb|CAA26231.1| G unnamed protein product [Mus musculus]

```

```

gb|AAA40539.1| G urokinase-type plasminogen activator [Mus musculus]
gb|AAI20710.1| G Plasminogen activator, urokinase [Mus musculus]

```

gb|AAI20714.1| **G** Plasminogen activator, urokinase [Mus musculus]
gb|EDL01484.1| **G** plasminogen activator, urokinase [Mus musculus]
dbj|BAH02680.1| urokinase-type plasminogen activator [Mammalian expression vect
 pmAlbEPintPlauGH]
 Length=433

GENE ID: 18792 Plau | plasminogen activator, urokinase [Mus musculus]
 (Over 100 PubMed links)

Score = 25.2 bits (52), Expect = 708
 Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 RSTGQC 7
 RSTGQC
 Sbjct 284 RSTGQC 290

>**gb|ACX36965.1|** middle S protein [Hepatitis B virus]
gb|ACX36975.1| middle S protein [Hepatitis B virus]
 Length=243

Score = 24.8 bits (51), Expect = 949
 Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8
 TSTGQCK
 Sbjct 133 TSTGQCK 139

>**gb|ACX36957.1|** middle S protein [Hepatitis B virus]
 Length=243

Score = 24.8 bits (51), Expect = 949
 Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8
 TSTGQCK
 Sbjct 133 TSTGQCK 139

>**gb|ABU97123.1|** S protein [Hepatitis B virus]
 Length=57

Score = 24.8 bits (51), Expect = 949
 Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8
 TSTGQCK
 Sbjct 9 TSTGQCK 15

>**gb|ABI17005.1|** surface antigen [Hepatitis B virus]
 Length=57

Score = 24.8 bits (51), Expect = 949
 Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8
 TSTGQCK
 Sbjct 9 TSTGQCK 15

>**dbj|BAG12008.1|** S protein [Hepatitis B virus]
 Length=254

Score = 24.8 bits (51), Expect = 949
 Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8
 TSTGQCK
 Sbjct 144 TSTGQCK 150

>**ref|XP_001450163.1|** **UG** hypothetical protein [Paramecium tetraurelia strain d4-
emb|CAK82766.1| **G** unnamed protein product [Paramecium tetraurelia]
 Length=2233

GENE ID: 5035948 GSPATT00017138001 | hypothetical protein
[Paramecium tetraurelia strain d4-2]

Score = 24.8 bits (51), Expect = 949
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8
Sbjct 1936 TSTGQCK 1942

>gb|AA59509.1| HBsAg [Hepatitis B virus]
Length=101

Score = 24.8 bits (51), Expect = 949
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8
Sbjct 5 TSTGQCK 11

>gb|AA59315.1| HBsAg [Hepatitis B virus]
Length=101

Score = 24.8 bits (51), Expect = 949
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8
Sbjct 5 TSTGQCK 11

>gb|AAA61740.1| 51C surface protein [Paramecium tetraurelia]
Length=2233

Score = 24.8 bits (51), Expect = 949
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8
Sbjct 1936 TSTGQCK 1942

>gb|AAW65562.1| HBsAg [Hepatitis B virus]
Length=226

Score = 24.8 bits (51), Expect = 949
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8
Sbjct 116 TSTGQCK 122

>gb|AAD13661.1| surface antigen [Hepatitis B virus]
Length=226

Score = 23.5 bits (48), Expect = 2294
Identities = 7/8 (87%), Positives = 7/8 (87%), Gaps = 0/8 (0%)

Query 1 RSTGQCK 8
Sbjct 115 RSTGQCK 122

>gb|ACB45647.1| truncated S protein [Hepatitis B virus]
Length=171

Score = 23.1 bits (47), Expect = 3077
Identities = 8/11 (72%), Positives = 8/11 (72%), Gaps = 3/11 (27%)

Query 1 RST---GQCK 8
Sbjct 112 RSTGQCK 122

>gb|ACB45646.1| truncated large S protein [Hepatitis B virus]
Length=345

Score = 23.1 bits (47), Expect = 3077
Identities = 8/11 (72%), Positives = 8/11 (72%), Gaps = 3/11 (27%)

Query 1 RSTST---GQCK 8
RSTST GQCK
Sbjct 286 RSTSTGTGQCK 296

>ref|XP_001750707.1| **G** hypothetical protein [Monosiga brevicollis MX1]
gb|EDQ84520.1| **G** predicted protein [Monosiga brevicollis MX1]
Length=1216

GENE ID: 5895935 MONBRDRAFT_30197 | hypothetical protein
[Monosiga brevicollis MX1]

Score = 23.1 bits (47), Expect = 3077
Identities = 8/11 (72%), Positives = 8/11 (72%), Gaps = 3/11 (27%)

Query 1 RISTGQ---CK 8
RISTGQ CK
Sbjct 451 RISTGQVIACK 461

>ref|XP_002092075.1| **G** GE11868 [Drosophila yakuba]
gb|EDW91787.1| **G** GE11868 [Drosophila yakuba]
Length=817

GENE ID: 6531266 Dyak\GE11868 | GE11868 gene product from transcript GE11868-RA
[Drosophila yakuba] (10 or fewer PubMed links)

Score = 22.7 bits (46), Expect = 4129
Identities = 7/8 (87%), Positives = 7/8 (87%), Gaps = 0/8 (0%)

Query 1 RISTGQCK 8
RISTGQ K
Sbjct 389 RISTGQSK 396

>gb|EFA75884.1| hypothetical protein PPL_10456 [Polysphondylium pallidum PN500]
Length=641

Score = 22.3 bits (45), Expect = 5541
Identities = 6/7 (85%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8
T+TGQCK
Sbjct 242 TATGQCK 248

Score = 19.7 bits (39), Expect = 32333
Identities = 6/7 (85%), Positives = 6/7 (85%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8
TS GQCK
Sbjct 158 TSDGQCK 164

>ref|YP_003006388.1| **G** Cof-like hydrolase [Dickeya zeae Ech1591]
gb|ACT08909.1| **G** Cof-like hydrolase [Dickeya zeae Ech1591]
Length=279

GENE ID: 8120965 Dd1591_4113 | Cof-like hydrolase [Dickeya zeae Ech1591]

Score = 22.3 bits (45), Expect = 5541
Identities = 6/7 (85%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 RISTGQC 7
RISTG+C
Sbjct 84 RISTGEC 90

>gb|EEE22595.1| BNR/Asp-box repeat domain-containing protein, putative [Toxoplasma gondii GT1]
gb|EEE31368.1| BNR/Asp-box repeat domain-containing protein, putative [Toxoplasma gondii VEG]

Length=962

Score = 22.3 bits (45), Expect = 5541
Identities = 6/7 (85%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 R1STGQC 7
R1STG+C
Sbjct 374 R1STGEC 380

>ref|XP_002368431.1| **G** sortilin, putative [Toxoplasma gondii ME49]
gb|EEB01291.1| **G** sortilin, putative [Toxoplasma gondii ME49]
Length=962

GENE ID: 7897795 **TGME49_090160** | sortilin, putative [Toxoplasma gondii ME49]
Score = 22.3 bits (45), Expect = 5541
Identities = 6/7 (85%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 R1STGQC 7
R1STG+C
Sbjct 374 R1STGEC 380

>ref|NP_001144615.1| **UG** hypothetical protein LOC100277631 [Zea mays]
gb|ACG41806.1| **G** hypothetical protein [Zea mays]
Length=496

GENE ID: 100277631 **LOC100277631** | hypothetical protein LOC100277631 [Zea mays]
(10 or fewer PubMed links)

Score = 22.3 bits (45), Expect = 5541
Identities = 6/7 (85%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 R1STGQC 7
R1STG+C
Sbjct 189 R1STGEC 195

>ref|XP_001742225.1| **G** hypothetical protein [Monosiga brevicollis MX1]
gb|EDQ92463.1| **G** predicted protein [Monosiga brevicollis MX1]
Length=1201

GENE ID: 5887979 **MONBRDRAFT_22150** | hypothetical protein
[Monosiga brevicollis MX1]

Score = 22.3 bits (45), Expect = 5541
Identities = 6/7 (85%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 R1STGQC 7
R1STG+C
Sbjct 41 R1STGEC 47

>ref|XP_001764053.1| **G** predicted protein [Physcomitrella patens subsp. patens]
gb|EDQ71192.1| **G** predicted protein [Physcomitrella patens subsp. patens]
Length=374

GENE ID: 5927198 **PHYPADRAFT_77455** | hypothetical protein
[Physcomitrella patens subsp. patens] (10 or fewer PubMed links)

Score = 22.3 bits (45), Expect = 5541
Identities = 6/7 (85%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 R1STGQC 7
RTS+GQC
Sbjct 189 RTSSGQC 195

>ref|YP_001669438.1| **G** FAD dependent oxidoreductase [Pseudomonas putida GB-1]
gb|ABY99102.1| **G** FAD dependent oxidoreductase [Pseudomonas putida GB-1]
Length=378

GENE ID: 5870995 PputGB1_3210 | FAD dependent oxidoreductase
[Pseudomonas putida GB-1]

Score = 22.3 bits (45), Expect = 5541
Identities = 6/7 (85%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 RTSTGQC 7
RTS+GQC
Sbjct 186 RTSSGQC 192

>ref|XP_001756901.1| **UG** predicted protein [Physcomitrella patens subsp. patens]
dbj|EAB39467.1| **G** putative alpha-glucosidase [Physcomitrella patens subsp. patens]
gb|EDQ78132.1| **G** predicted protein [Physcomitrella patens subsp. patens]
Length=916

GENE ID: 5920253 PHYPADRAFT_205099 | hypothetical protein
[Physcomitrella patens subsp. patens] (10 or fewer PubMed links)

Score = 22.3 bits (45), Expect = 5541
Identities = 6/7 (85%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 RTSTGQC 7
RTSTG+C
Sbjct 146 RTSTGEC 152

>ref|XP_638862.1| **G** hypothetical protein DDB_G0283853 [Dictyostelium discoideum]
gb|EAL65541.1| **G** hypothetical protein DDB_G0283853 [Dictyostelium discoideum AX]
Length=628

GENE ID: 8624260 DDB_G0283853 | hypothetical protein
[Dictyostelium discoideum AX4] (10 or fewer PubMed links)

Score = 22.3 bits (45), Expect = 5541
Identities = 6/7 (85%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8
T+IGQCK
Sbjct 287 TINTGQCK 293

>ref|XP_638860.1| **G** hypothetical protein DDB_G0283869 [Dictyostelium discoideum]
gb|EAL65549.1| **G** hypothetical protein DDB_G0283869 [Dictyostelium discoideum AX]
Length=1141

GENE ID: 8624258 DDB_G0283869 | hypothetical protein
[Dictyostelium discoideum AX4] (10 or fewer PubMed links)

Score = 22.3 bits (45), Expect = 5541
Identities = 6/7 (85%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8
T+IGQCK
Sbjct 798 TINTGQCK 804

>ref|XP_638863.1| **UG** hypothetical protein DDB_G0283787 [Dictyostelium discoideum]
gb|EAL65508.1| **G** hypothetical protein DDB_G0283787 [Dictyostelium discoideum AX]
Length=1064

GENE ID: 8624261 DDB_G0283787 | hypothetical protein
[Dictyostelium discoideum AX4] (10 or fewer PubMed links)

Score = 22.3 bits (45), Expect = 5541
Identities = 6/7 (85%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8
T+IGQCK
Sbjct 728 TINTGQCK 734

>gb|EFB29915.1| hypothetical protein PANDA 005925 [Ailuropoda melanoleuca]

Length=2869

Score = 21.8 bits (44), Expect = 7434
 Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
 TSTGQC
 Sbjct 1842 TSTGQC 1847

>**gb|EFA82002.1|** hypothetical protein PPL_05237 [Polysphondylium pallidum PN500]
 Length=1715

Score = 21.8 bits (44), Expect = 7434
 Identities = 6/7 (85%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8
 TSTG+CK
 Sbjct 990 TSTGECK 996

>**gb|EFA82001.1|** carbohydrate-binding domain-containing protein [Polysphondylium pallidum PN500]
 Length=705

Score = 21.8 bits (44), Expect = 7434
 Identities = 6/7 (85%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8
 TSTG+CK
 Sbjct 527 TSTGECK 533

>**ref|ZP_06141814.1|** pectinesterase [Ruminococcus flavefaciens FD-1]
 Length=374

Score = 21.8 bits (44), Expect = 7434
 Identities = 6/7 (85%), Positives = 6/7 (85%), Gaps = 0/7 (0%)

Query 1 RISTGQC 7
 RT TGQC
 Sbjct 27 RIGTGQC 33

>**emb|CBH16504.1|** periodic tryptophan protein 2, putative; predicted WD40 repeat protein [Trypanosoma brucei gambiense DAL972]
 Length=939

Score = 21.8 bits (44), Expect = 7434
 Identities = 6/7 (85%), Positives = 6/7 (85%), Gaps = 0/7 (0%)

Query 1 RISTGQC 7
 R STGQC
 Sbjct 432 RASTGQC 438

>**ref|XP_002444714.1|** **G** hypothetical protein SORBIDRAFT_07g026515 [Sorghum bicolor]
gb|EES14209.1| **G** hypothetical protein SORBIDRAFT_07g026515 [Sorghum bicolor]
 Length=394

GENE ID: 8060966 SORBIDRAFT_07g026515 | hypothetical protein [Sorghum bicolor]
 (10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434
 Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
 TSTGQC
 Sbjct 150 TSTGQC 155

>**ref|XP_002578344.1|** **UG** transcription initiation factor brfl [Schistosoma mansoni]
emb|CAZ34582.1| **G** transcription initiation factor brfl, putative [Schistosoma mansonii]
 Length=770

GENE ID: 8348817 Smp_071570 | transcription initiation factor brfl
 [Schistosoma mansoni] (10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
TSTGQC
Sbjct 43 TSTGQC 48

>ref|YP_002756665.1| **G** lipoprotein [Escherichia coli]

gb|ACL52052.1| **G** lipoprotein [Escherichia coli]
Length=356

GENE ID: 7701488 p026VIR_p114 | lipoprotein [Escherichia coli]

Score = 21.8 bits (44), Expect = 7434
Identities = 6/7 (85%), Positives = 6/7 (85%), Gaps = 0/7 (0%)

Query 1 RISTGQC 7
RISTGQC
Sbjct 340 RISTGQC 346

>ref|YP_002731228.1| **G** cytochrome C family protein [Persephonella marina EX-H1]

gb|ACO04288.1| **G** cytochrome C family protein [Persephonella marina EX-H1]
Length=326

GENE ID: 7675008 PERMA_1460 | cytochrome C family protein
[Persephonella marina EX-H1] (10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
TSTGQC
Sbjct 226 TSTGQC 231

>ref|XP_001013897.2| **G** hypothetical protein TTHERM_01486710 [Tetrahymena thermop

gb|EAR93652.2| **G** hypothetical protein TTHERM_01486710 [Tetrahymena thermophila
SB210]
Length=2346

GENE ID: 7823083 TTHERM_01486710 | hypothetical protein
[Tetrahymena thermophila]

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
TSTGQC
Sbjct 769 TSTGQC 774

>ref|ZP_03726320.1| DNA topoisomerase (ATP-hydrolyzing) [Opitutaceae bacterium T

gb|EEG19652.1| DNA topoisomerase (ATP-hydrolyzing) [Opitutaceae bacterium TAV2]
Length=788

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
TSTGQC
Sbjct 493 TSTGQC 498

>gb|EEE55720.1| hypothetical protein OsJ_04192 [Oryza sativa Japonica Group]
Length=904

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 3 STGQCK 8
STGQCK
Sbjct 676 STGQCK 681

>ref|XP_002290185.1| **G** predicted protein [Thalassiosira pseudonana CCMP1335]
 gb|EED91937.1| **G** predicted protein [Thalassiosira pseudonana CCMP1335]
 Length=2183

GENE ID: 7449574 THAPSDRAFT_22658 | hypothetical protein
 [Thalassiosira pseudonana CCMP1335] (10 or fewer PubMed links)
 Score = 21.8 bits (44), Expect = 7434
 Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
 TSTGQC
 Sbjct 1235 TSTGQC 1240

>ref|YP_002418785.1| **G** putative lipoprotein [Escherichia coli]
 emb|CAQ87359.1| **G** putative lipoprotein [Escherichia coli]
 Length=355

GENE ID: 7872117 pill | putative lipoprotein [Escherichia coli ED1a]
 Score = 21.8 bits (44), Expect = 7434
 Identities = 6/7 (85%), Positives = 6/7 (85%), Gaps = 0/7 (0%)

Query 1 RSTGQC 7
 RST QC
 Sbjct 339 RTSTAQC 345

>ref|XP_002412137.1| **G** hypothetical protein IscW_ISCW011495 [Ixodes scapularis]
 gb|EEC14721.1| **G** hypothetical protein IscW_ISCW011495 [Ixodes scapularis]
 Length=103

GENE ID: 8036937 IscW_ISCW011495 | hypothetical protein [Ixodes scapularis]
 Score = 21.8 bits (44), Expect = 7434
 Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 3 STGQCK 8
 STGQCK
 Sbjct 37 STGQCK 42

>ref|XP_002598165.1| **G** hypothetical protein BRAFLDRAFT_123314 [Branchiostoma flo
 gb|EEN54177.1| **G** hypothetical protein BRAFLDRAFT_123314 [Branchiostoma floridae]
 Length=700

GENE ID: 7231595 BRAFLDRAFT_123314 | hypothetical protein
 [Branchiostoma floridae] (10 or fewer PubMed links)
 Score = 21.8 bits (44), Expect = 7434
 Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 3 SIGQCK 8
 SIGQCK
 Sbjct 608 SIGQCK 613

>ref|XP_002612022.1| **UG** hypothetical protein BRAFLDRAFT_86993 [Branchiostoma fl
 gb|EEN68031.1| **G** hypothetical protein BRAFLDRAFT_86993 [Branchiostoma floridae]
 Length=1268

GENE ID: 7243150 BRAFLDRAFT_86993 | hypothetical protein
 [Branchiostoma floridae] (10 or fewer PubMed links)
 Score = 21.8 bits (44), Expect = 7434
 Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
 TSTGQC
 Sbjct 270 TSTGQC 275

>ref|XP_002613108.1| **UG** hypothetical protein BRAFLDRAFT_89993 [Branchiostoma fl
gb|EEN69117.1| **G** hypothetical protein BRAFLDRAFT_89993 [Branchiostoma floridae]
Length=219

GENE ID: 7209147 BRAFLDRAFT_89993 | hypothetical protein
[Branchiostoma floridae] (10 or fewer PubMed links)
Score = 21.8 bits (44), Expect = 7434
Identities = 6/8 (75%), Positives = 7/8 (87%), Gaps = 0/8 (0%)

Query 1 RTSTGGCK 8
RT +GQCK
Sbjct 36 RTGSGGCK 43

>ref|XP_002124394.1| **G** PREDICTED: similar to integrin beta Hrl [Ciona intestinal
Length=840

GENE ID: 100180214 LOC100180214 | similar to integrin beta Hrl
[Ciona intestinalis]
Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 3 SIGQCK 8
SIGQCK
Sbjct 731 SIGQCK 736

>dbj|BAG65498.1| **G** unnamed protein product [Homo sapiens]
Length=1149

GENE ID: 2200 FBN1 | fibrillin 1 [Homo sapiens] (Over 100 PubMed links)
Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
TSTGQC
Sbjct 732 TSTGQC 737

>gb|AAI66315.1| **G** LOC100158602 protein [Xenopus (Silurana) tropicalis]
Length=883

GENE ID: 100158602 LOC100158602 | hypothetical protein LOC100158602
[Xenopus (Silurana) tropicalis] (10 or fewer PubMed links)
Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 3 SIGQCK 8
SIGQCK
Sbjct 793 SIGQCK 798

>ref|XP_001912476.1| **G** unnamed protein product [Podospora anserina]
emb|CAP59957.1| **G** unnamed protein product [Podospora anserina]
Length=588

GENE ID: 6197588 PODANSg09524 | hypothetical protein
[Podospora anserina DSM 980]
Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
TSTGQC
Sbjct 388 TSTGQC 393

>ref|XP_001907985.1| **G** unnamed protein product [Podospora anserina]

emb|CAP68658.1| **G** unnamed protein product [Podospira anserina]
Length=111

GENE ID: 6192331 PODANSg5020 | hypothetical protein
[Podospira anserina DSM 980]

Score = 21.8 bits (44), Expect = 7434
Identities = 6/8 (75%), Positives = 6/8 (75%), Gaps = 0/8 (0%)

Query 1 RTSTGQCK 8
RIST CK
Sbjct 60 RISTSHCK 67

>**ref|XP_001770300.1|** **UG** predicted protein [Physcomitrella patens subsp. patens]
gb|EDQ64975.1| **G** predicted protein [Physcomitrella patens subsp. patens]
Length=559

GENE ID: 5933481 PHYPADRAFT_84461 | hypothetical protein
[Physcomitrella patens subsp. patens] (10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 3 STGQCK 8
SIGQCK
Sbjct 304 STGQCK 309

>**ref|XP_001775575.1|** **UG** p300/CBP acetyltransferase-related protein [Physcomitre
subsp. patens]
gb|EDQ59658.1| **G** p300/CBP acetyltransferase-related protein [Physcomitrella pat
subsp. patens]
Length=1617

GENE ID: 5938778 HAC1501 | p300/CBP acetyltransferase-related protein
[Physcomitrella patens subsp. patens] (10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434
Identities = 6/7 (85%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8
TSTG+CK
Sbjct 1232 TSTGECK 1238

>**ref|XP_001785357.1|** **UG** p300/CBP acetyltransferase-related protein [Physcomitre
subsp. patens]
gb|EDQ49842.1| **G** p300/CBP acetyltransferase-related protein [Physcomitrella pat
subsp. patens]
Length=1082

GENE ID: 5948557 HAC1502 | p300/CBP acetyltransferase-related protein
[Physcomitrella patens subsp. patens] (10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434
Identities = 6/7 (85%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8
TSTG+CK
Sbjct 697 TSTGECK 703

>**ref|ZP_02094454.1|** hypothetical protein PEPMIC_01220 [Parvimonas micra ATCC 332
gb|EDP23416.1| hypothetical protein PEPMIC_01220 [Parvimonas micra ATCC 33270]
Length=324

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 3 STGQCK 8
STGQCK
Sbjct 93 STGQCK 98

>ref|XP_963736.2| **UG** hypothetical protein NCU03244 [Neurospora crassa OR74A]
 gb|EAA34500.2| **G** conserved hypothetical protein [Neurospora crassa OR74A]
 Length=531

GENE ID: 3879885 NCU03244 | hypothetical protein [Neurospora crassa OR74A]
 (10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434
 Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
 TSTGQC
 Sbjct 343 TSTGQC 348

>ref|XP_001502309.1| **UG** PREDICTED: fibrillin 1 [Equus caballus]
 Length=2871

GENE ID: 100055741 FBN1 | fibrillin 1 [Equus caballus]

Score = 21.8 bits (44), Expect = 7434
 Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
 TSTGQC
 Sbjct 1842 TSTGQC 1847

>ref|ZP_01894398.1| hypothetical protein MDG893_13589 [Marinobacter algicola DG8
 gb|EDM47477.1| hypothetical protein MDG893_13589 [Marinobacter algicola DG893]
 Length=137

Score = 21.8 bits (44), Expect = 7434
 Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
 TSTGQC
 Sbjct 116 TSTGQC 121

>gb|EDL80069.1| **G** fibrillin 1, isoform CRA_a [Rattus norvegicus]
 gb|EDL80070.1| **G** fibrillin 1, isoform CRA_a [Rattus norvegicus]
 Length=2872

GENE ID: 83727 Fbn1 | fibrillin 1 [Rattus norvegicus]
 (10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434
 Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
 TSTGQC
 Sbjct 1843 TSTGQC 1848

>gb|EDL80071.1| **G** fibrillin 1, isoform CRA_b [Rattus norvegicus]
 Length=2807

GENE ID: 83727 Fbn1 | fibrillin 1 [Rattus norvegicus]
 (10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434
 Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
 TSTGQC
 Sbjct 1778 TSTGQC 1783

>gb|EDL28139.1| **G** fibrillin 1, isoform CRA_a [Mus musculus]
 gb|EDL28140.1| **G** fibrillin 1, isoform CRA_b [Mus musculus]
 Length=2873

GENE ID: 14118 Fbn1 | fibrillin 1 [Mus musculus] (Over 100 PubMed links)

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
TSTGQC
Sbjct 1844 TSTGQC 1849

>ref|XP_001393188.1| **G** hypothetical protein An08g10840 [Aspergillus niger]
emb|CAK45757.1| **G** hypothetical protein [Aspergillus niger]
Length=329

GENE ID: 4983398 An08g10840 | hypothetical protein
[Aspergillus niger CBS 513.88] (10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
TSTGQC
Sbjct 292 TSTGQC 297

>ref|XP_001369848.1| **UG** PREDICTED: hypothetical protein [Monodelphis domestica]
Length=2871

GENE ID: 100025769 LOC100025769 | hypothetical protein LOC100025769
[Monodelphis domestica]

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
TSTGQC
Sbjct 1843 TSTGQC 1848

>gb|EAY76601.1| hypothetical protein OsI_04550 [Oryza sativa Indica Group]
Length=895

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 3 STGQCK 8
STGQCK
Sbjct 667 STGQCK 672

>ref|XP_001443583.1| **UG** hypothetical protein [Paramecium tetraurelia strain d4-emb|CAK76186.1| **G** unnamed protein product [Paramecium tetraurelia]
Length=2350

GENE ID: 5029368 GSPATT00011759001 | hypothetical protein
[Paramecium tetraurelia strain d4-2]

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
TSTGQC
Sbjct 2043 TSTGQC 2048

>ref|ZP_01693530.1| conserved protein [Microscilla marina ATCC 23134]
gb|EAY25518.1| conserved protein [Microscilla marina ATCC 23134]
Length=193

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
TSTGQC
Sbjct 98 TSTGQC 103

>gb|EAW77353.1| **G** fibrillin 1 (Marfan syndrome), isoform CRA_a [Homo sapiens]
Length=2869

GENE ID: 2200 FBN1 | fibrillin 1 [Homo sapiens] (Over 100 PubMed links)

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
TSTGQC
Sbjct 1842 TSTGQC 1847

>ref|NP_000129.3| **G** fibrillin 1 precursor [Homo sapiens]

sp|P35555.2|FBN1 HUMAN **G** RecName: Full=Fibrillin-1; Flags: Precursor

gb|EAW77354.1| **G** fibrillin 1 (Marfan syndrome), isoform CRA_b [Homo sapiens]

gb|AAI46855.1| **G** Fibrillin 1 [Homo sapiens]

gb|ACZ58372.1| fibrillin 1 [Homo sapiens]
Length=2871

GENE ID: 2200 FBN1 | fibrillin 1 [Homo sapiens] (Over 100 PubMed links)

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
TSTGQC
Sbjct 1842 TSTGQC 1847

>ref|NP_032019.2| **UG** fibrillin 1 [Mus musculus]

emb|CAM22806.1| **G** fibrillin 1 [Mus musculus]

emb|CAM17722.1| **G** fibrillin 1 [Mus musculus]
Length=2873

GENE ID: 14118 Fbn1 | fibrillin 1 [Mus musculus] (Over 100 PubMed links)

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
TSTGQC
Sbjct 1844 TSTGQC 1849

>ref|YP_856076.1| **G** drug/metabolite exporter family transporter [Aeromonas hydrophila subsp. hydrophila ATCC 7966]

gb|ABK39216.1| **G** transporter, 10 TMS drug/metabolite exporter (DME) family [Aeromonas hydrophila subsp. hydrophila ATCC 7966]
Length=293

GENE ID: 4487228 AHA_1538 | drug/metabolite exporter family transporter [Aeromonas hydrophila subsp. hydrophila ATCC 7966] (10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434
Identities = 6/7 (85%), Positives = 6/7 (85%), Gaps = 0/7 (0%)

Query 1 RSTGQC 7
R STGQC
Sbjct 284 RASTGQC 290

>ref|XP_001149266.1| **UG** PREDICTED: fibrillin 1 [Pan troglodytes]
Length=3004

GENE ID: 453411 FBN1 | fibrillin 1 [Pan troglodytes]

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
TSTGQC

Sbjct 1975 TSTGQC 1980

>ref|NP_001044899.1| **UG** Os01g0865600 [Oryza sativa (japonica cultivar-group)]
Length=921

GENE ID: 4324795 Os01g0865600 | Os01g0865600 [Oryza sativa Japonica Group]
(10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 3 STGQCK 8
STGQCK
Sbjct 693 STGQCK 698

>ref|XP_397600.3| **UG** PREDICTED: similar to family with sequence similarity 48,
A isoform b [Apis mellifera]
Length=1078

GENE ID: 410031 LOC410031 | similar to family with sequence similarity 48,
member A isoform b [Apis mellifera]

Score = 21.8 bits (44), Expect = 7434
Identities = 6/7 (85%), Positives = 6/7 (85%), Gaps = 0/7 (0%)

Query 1 RTSTGQC 7
R STGQC
Sbjct 1005 RASTGQC 1011

>ref|XP_392100.3| **UG** PREDICTED: similar to CG16791-PA [Apis mellifera]
Length=452

GENE ID: 408555 LOC408555 | similar to CG16791-PA [Apis mellifera]
(10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
TSTGQC
Sbjct 419 TSTGQC 424

>ref|XP_001100608.1| **UG** PREDICTED: estrogen-related receptor beta isoform 2 [Ma
Length=454

GENE ID: 703799 ESRRB | estrogen-related receptor beta [Macaca mulatta]

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
TSTGQC
Sbjct 161 TSTGQC 166

>ref|XP_001113107.1| **UG** PREDICTED: similar to fibrillin 1 precursor [Macaca mul
Length=2871

GENE ID: 714451 LOC714451 | similar to fibrillin 1 precursor [Macaca mulatta]


Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
TSTGQC
Sbjct 1842 TSTGQC 1847

>ref|ZP_01306957.1| hypothetical protein RED65_16411 [Oceanobacter sp. RED65]
gb|EAT12438.1| hypothetical protein RED65_16411 [Oceanobacter sp. RED65]
Length=135

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)


Query 2 TSTGQC 7
TSTGQC
Sbjct 109 TSTGQC 114

>ref|XP_861706.1|  PREDICTED: similar to Fibrillin-1 precursor isoform 3 [Canis familiaris]
Length=2417

GENE ID: 478293 FBN1 | fibrillin 1 [Canis lupus familiaris]

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
TSTGQC
Sbjct 1842 TSTGQC 1847

>ref|XP_535468.2|  PREDICTED: similar to Fibrillin-1 precursor isoform 1 [Canis familiaris]
Length=2871

GENE ID: 478293 FBN1 | fibrillin 1 [Canis lupus familiaris]

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
TSTGQC
Sbjct 1842 TSTGQC 1847

>dbj|BAD92077.1|  fibrillin 1 variant [Homo sapiens]
Length=830

GENE ID: 2200 FBN1 | fibrillin 1 [Homo sapiens] (Over 100 PubMed links)

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
TSTGQC
Sbjct 277 TSTGQC 282

>dbj|BAD81907.1| bHLH transcription factor-like protein [Oryza sativa Japonica Group]

dbj|BAG90720.1| unnamed protein product [Oryza sativa Japonica Group]
dbj|BAF06813.2| Os0lg0865600 [Oryza sativa Japonica Group]
Length=904

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)


Query 3 STGQCK 8
STGQCK
Sbjct 676 STGQCK 681

>gb|AAT94187.1| PilL [Escherichia coli]
Length=356

Score = 21.8 bits (44), Expect = 7434
Identities = 6/7 (85%), Positives = 6/7 (85%), Gaps = 0/7 (0%)

Query 1 RSTGQC 7
RSTGQC
Sbjct 340 RSTGQC 346

>ref|YP_308679.1|  lipoprotein [Escherichia coli]

gb|AAL18827.2|  Lipoprotein [Escherichia coli]

Length=356

GENE ID: 3654428 pill | lipoprotein [Escherichia coli]
(10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434
Identities = 6/7 (85%), Positives = 6/7 (85%), Gaps = 0/7 (0%)

Query 1 RTSTGQC 7
RTST QC
Sbjct 340 RTSTAQC 346

>gb|AAL05516.1|AF399919_3 Pill [Escherichia coli]
Length=357

Score = 21.8 bits (44), Expect = 7434
Identities = 6/7 (85%), Positives = 6/7 (85%), Gaps = 0/7 (0%)

Query 1 RTSTGQC 7
RTST QC
Sbjct 341 RTSTAQC 347

>emb|CAD19195.1| novel protein similar to MHC class II beta chain [Danio rerio]
Length=249

GENE ID: 368615 si:busml-194e12.12 | si:busml-194e12.12 [Danio rerio]
(10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 3 STGQCK 8
STGQCK
Sbjct 244 STGQCK 249

>ref|XP_001030843.1| hypothetical protein THERM_01006510 [Tetrahymena thermop
gb|EAR83180.1| hypothetical protein THERM_01006510 [Tetrahymena thermophila
SB210]
Length=1588

GENE ID: 7842955 THERM_01006510 | hypothetical protein
[Tetrahymena thermophila]

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 3 STGQCK 8
STGQCK
Sbjct 287 STGQCK 292

>gb|AAC62317.1| mutant fibrillin-1 [Mus musculus]
Length=3857

GENE ID: 14118 Fbn1 | fibrillin 1 [Mus musculus] (Over 100 PubMed links)

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
TSTGQC
Sbjct 2828 TSTGQC 2833

>gb|AAA64217.1| fibrillin-1 [Mus musculus]
Length=2873

GENE ID: 14118 Fbn1 | fibrillin 1 [Mus musculus] (Over 100 PubMed links)

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7

Sbjct 1844 TSTGQC 1849
TSTGQC

>ref|XP_861733.1| **G** PREDICTED: similar to Fibrillin-1 precursor isoform 4 [Canis familiaris]
Length=2816

GENE ID: 478293 FBN1 | fibrillin 1 [Canis lupus familiaris]

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
TSTGQC
Sbjct 1842 TSTGQC 1847

>ref|XP_861765.1| **G** PREDICTED: similar to Fibrillin-1 precursor isoform 5 [Canis familiaris]
Length=2804

GENE ID: 478293 FBN1 | fibrillin 1 [Canis lupus familiaris]

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
TSTGQC
Sbjct 1787 TSTGQC 1792

>ref|XP_861792.1| **G** PREDICTED: similar to Fibrillin-1 precursor isoform 6 [Canis familiaris]
Length=2872

GENE ID: 478293 FBN1 | fibrillin 1 [Canis lupus familiaris]

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
TSTGQC
Sbjct 1843 TSTGQC 1848

>ref|NP_114013.1| **UG** fibrillin 1 [Rattus norvegicus]
gb|AAD34438.1| **G** fibrillin-1 [Rattus norvegicus]
Length=2872

GENE ID: 83727 Fbn1 | fibrillin 1 [Rattus norvegicus]
(10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
TSTGQC
Sbjct 1843 TSTGQC 1848

>dbj|BAD16739.1| **G** fibrillin 1 [Homo sapiens]
Length=2871

GENE ID: 2200 FBN1 | fibrillin 1 [Homo sapiens] (Over 100 PubMed links)

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
TSTGQC
Sbjct 1842 TSTGQC 1847

>ref|XP_002633929.1| **G** C. briggsae CBR-LAM-1 protein [Caenorhabditis briggsae]

emb|CAP37137.1| **C** C. briggsae CBR-LAM-1 protein [Caenorhabditis briggsae]
Length=1265

GENE ID: 8575925 Cbr-lam-1 | C. briggsae CBR-LAM-1 protein
[Caenorhabditis briggsae]

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 3 TSTGQCK 8
Sbjct 587 TSTGQCK 592

>**ref|NP_001001771.1|** **UG** fibrillin 1 precursor [Sus scrofa]
sp|Q9TV36.1|FBN1_PIG **C** RecName: Full=Fibrillin-1; Flags: Precursor
gb|AAD50328.1|AF073800.1 **C** fibrillin-1 precursor [Sus scrofa]
Length=2871

GENE ID: 414836 FBN1 | fibrillin 1 [Sus scrofa] (10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
Sbjct 1842 TSTGQC 1847

>**prf||1713408A** fibrillin
Length=1973

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
Sbjct 944 TSTGQC 949

>**sp|Q61554.1|FBN1_MOUSE** **C** RecName: Full=Fibrillin-1; Flags: Precursor
gb|AAA56840.1| **C** fibrillin [Mus musculus]
Length=2871

GENE ID: 14118 Fbn1 | fibrillin 1 [Mus musculus] (Over 100 PubMed links)

Score = 21.8 bits (44), Expect = 7434
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7
Sbjct 1842 TSTGQC 1847

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